I. AMENDMENT

In the Claims:

Please replace the claims with the following listings of claims:

1.   to 5. (Canceled).

6.   (Currently Amended) A diagnostic system for quantitating the individual contribution of
     a mutation or combination of mutations to a drug resistance phenotype exhibited by an
     HIV strain, said system comprising:

     ~~means for obtaining a genetic sequence of said HIV strain;~~

     ~~means for identifying the mutation pattern in said genetic sequence as compared to wild~~

     ~~type HIV; and~~

     computer means for predicting the fold resistance exhibited by said HIV strain using a

     method comprising the steps of:

     ~~1)~~ performing a linear regression analysis using data from a dataset of matching
     genotypes and phenotypes, wherein the log fold resistance, pFR, of each said HIV strain
     is modeled as the sum of all ~~the~~ individual resistance contributions for each of said
     mutations or combinations of mutations that occur in HIV according to the following
     equation;

     $$pFR = \beta_A M_A + \beta_B M_B + \beta_n M_n + \cdots + \beta_Z M_Z + \varepsilon$$

     wherein each said individual resistance contribution is calculated by multiplying a
     mutation factor, M_A, M_B, ..., M_Z, for each of said mutation or combination of
     mutations by a resistance coefficient β_A, β_B, ..., β_Z;

     wherein for a combination of mutations, said mutation factor M_n represents the co-
     occurrence of one mutation with other one or more mutations and said coefficient β_n
     represents the synergy or antagonism between said one mutation with said other one or
     more mutations;

     wherein said mutation factor assigned to each said mutation or combination of mutations
     reflects the degree to which said mutation or combination of mutations is present in said
     HIV strain and, if present, to which degree said mutation is present in a mixture;

     wherein each said resistance coefficient reflects the contribution of said mutation or
     combination of mutations to said fold resistance exhibited by said strain;

     wherein the error term ε, represents the difference between a modeled prediction and an
     experimentally determined measurement;

~~2)~~when pFR contains a censored value, said method further comprising replacing ~~the~~ said pFR containing said censored value in said data from said dataset of matching genotype and phenotype by a maximum likelihood estimation;

wherein ~~for each iteration of said linear regression,~~ said maximum likelihood estimation is generated according to the following steps:

a) calculating a linear regression model without said censored values;

for each said pFR containing said censored value, using a phenotypic measured value V_0 as said pFR of said data of said dataset of matching genotypes and phenotypes ~~as if the censor was " = ", when a result is expressed as −log *FR* < 4, V_0 is treated as −log *FR* =4~~;

~~c)~~ using ~~the~~ a prediction P from said linear regression model, wherein ~~to apply either~~:

i) when ~~said phenotypic value is smaller than said range, a '<' censor is applied to said value~~censor of said censored value is '<':

~~i~~a) $P < V_0 − 0.798\ \sigma$ (center of gravity of half Gaussian distribution)

Remove V_0 value from a training data for ~~the next iteration~~ following step b

~~ii~~b) $V_0 − 0.798\ \sigma \le P < V_0$

Use V' for V_0 value, wherein $V' = V_0 − 0.798\ \sigma$ for ~~the next iteration~~ following step b

~~iii~~c) $V_0 \le P$

Use V' for V_0 vlaue, wherein V' is center of gravity of tail (<V) of a normal distribution N (P, σ) as value for ~~the next iteration~~ following step b

ii) when ~~said phenotypic value is higher than said range, a '>' censor is applied to said value V_0~~censor of said censored value is '>':

~~i~~a) $P > V_0 + 0.798\ \sigma$ (center of gravity of half Gaussian distribution)

Remove V_0 value from training data for ~~the next iteration~~ following step b

i~~i~~b) $V_0 + 0.798\ \sigma \ge P > V_0$

Use V' for V_0 value, wherein $V' = V_0 − 0.798\ \sigma$ for ~~the next iteration~~ following step b

ii~~i~~c) $V_0 \ge P$

Use <u>V' for V$_0$ value, wherein</u> V' center of gravity of tail (>V) of a normal distribution N (P, σ) as value for ~~the next iteration~~ <u>following step b</u>;

b) <u>re-</u>calculating ~~as~~<u>said</u> linear regression model ~~and for said censored values in said linear regression model, either remove the data-point from the training set, or use V' instead of the censored phenotype measurement, as described in step c)~~;

c) reiterating steps b) to ~~d~~<u>c</u>) until ~~the prediction~~<u>said model </u>converges;

thereby quantitating the individual contribution of said mutation or combination of mutations to said drug resistance phenotype exhibited by said HIV strain.

7. to 16. (Canceled).